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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=10; day=23; hr=16; min=48; sec=47; ms=752;
]

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Application No: 10573601

Version No: 2.1

Input Set:

Output Set:

Started: 2008-10-23 16:46:51.257

Finished: 2008-10-23 16:46:55.642

Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 385 ms

Total Warnings: 4

Total Errors: 20

No. of SeqIDs Defined: 6

Actual SeqID Count: 6

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
E 257	Invalid sequence data feature in <221> in SEQ ID (4)
E 257	Invalid sequence data feature in <221> in SEQ ID (4)
E 257	Invalid sequence data feature in <221> in SEQ ID (4)
E 257	Invalid sequence data feature in <221> in SEQ ID (4)
E 257	Invalid sequence data feature in <221> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 257	Invalid sequence data feature in <221> in SEQ ID (5)
E 257	Invalid sequence data feature in <221> in SEQ ID (5)
E 257	Invalid sequence data feature in <221> in SEQ ID (5)
E 257	Invalid sequence data feature in <221> in SEQ ID (5)
E 257	Invalid sequence data feature in <221> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 257	Invalid sequence data feature in <221> in SEQ ID (6)

Input Set:

Output Set:

Started: 2008-10-23 16:46:51.257
Finished: 2008-10-23 16:46:55.642
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Total Warnings: 4
Total Errors: 20
No. of SeqIDs Defined: 6
Actual SeqID Count: 6

Error code	Error Description
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E 257	Invalid sequence data feature in <221> in SEQ ID (6)
E 257	Invalid sequence data feature in <221> in SEQ ID (6)
E 257	Invalid sequence data feature in <221> in SEQ ID (6) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> HANSSON, HANS-ARNE
JENNISCHE, EVA
LANGE, STEFAN
LON-NROTH, IVAR
ERIKSSON, PETER
PERSSON, ANDERS

<120> NOVEL USE OF ANTISECRETORY FACTOR

<130> 1003301-000258

<140> 10/573,601

<141> 2006-08-11

<150> PCT/SE04/001369

<151> 2004-09-24

<150> GB 0322645.3

<151> 2003-09-26

<160> 6

<170> PatentIn Ver. 3.3

<210> 1

<211> 382

<212> PRT

<213> Homo sapiens

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Arg	Asn	Gly	Asp	Phe	Leu	Pro	Thr	Arg	Leu	Gln	Ala	Gln	Gln	Asp	Ala
		20						25					30		

Val	Asn	Ile	Val	Cys	His	Ser	Lys	Thr	Arg	Ser	Asn	Pro	Glu	Asn	Asn
		35					40				45				

Val	Gly	Leu	Ile	Thr	Leu	Ala	Asn	Asp	Cys	Glu	Val	Leu	Thr	Thr	Leu
	50					55					60				

Thr	Pro	Asp	Thr	Gly	Arg	Ile	Leu	Ser	Lys	Leu	His	Thr	Val	Gln	Pro
65					70					75				80	

Lys	Gly	Lys	Ile	Thr	Phe	Cys	Thr	Gly	Ile	Arg	Val	Ala	His	Leu	Ala
			85					90						95	

Leu	Lys	His	Arg	Gln	Gly	Lys	Asn	His	Lys	Met	Arg	Ile	Ile	Ala	Phe
			100				105						110		

Val	Gly	Ser	Pro	Val	Glu	Asp	Asn	Glu	Lys	Asp	Leu	Val	Lys	Leu	Ala
		115					120					125			

Lys	Arg	Leu	Lys	Lys	Glu	Lys	Val	Asn	Val	Asp	Ile	Ile	Asn	Phe	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

130	135	140																	
Glu	Glu	Glu	Val	Asn	Thr	Glu	Lys	Leu	Thr	Ala	Phe	Val	Asn	Thr	Leu				
145					150					155					160				
Asn	Gly	Lys	Asp	Gly	Thr	Gly	Ser	His	Leu	Val	Thr	Val	Pro	Pro	Gly				
				165					170						175				
Pro	Ser	Leu	Ala	Asp	Ala	Leu	Ile	Ser	Ser	Pro	Ile	Leu	Ala	Gly	Glu				
			180					185						190					
Gly	Gly	Ala	Met	Leu	Gly	Leu	Gly	Ala	Ser	Asp	Phe	Glu	Phe	Gly	Val				
	195						200					205							
Asp	Pro	Ser	Ala	Asp	Pro	Glu	Leu	Ala	Leu	Ala	Leu	Arg	Val	Ser	Met				
	210					215					220								
Glu	Glu	Gln	Arg	His	Ala	Gly	Gly	Gly	Ala	Arg	Arg	Ala	Ala	Arg	Ala				
225					230					235					240				
Ser	Ala	Ala	Glu	Ala	Gly	Ile	Ala	Thr	Thr	Gly	Thr	Glu	Asp	Ser	Asp				
				245					250					255					
Asp	Ala	Leu	Leu	Lys	Met	Thr	Ile	Ser	Gln	Gln	Glu	Phe	Gly	Arg	Thr				
		260						265					270						
Gly	Leu	Pro	Asp	Leu	Ser	Ser	Ser	Thr	Glu	Glu	Glu	Glu	Ile	Ala	Tyr				
	275						280					285							
Ala	Met	Gln	Met	Ser	Leu	Gln	Gly	Ala	Glu	Phe	Gly	Gln	Ala	Glu	Ser				
	290					295					300								
Ala	Asp	Ile	Asp	Ala	Ser	Ser	Ala	Met	Asp	Thr	Ser	Glu	Pro	Ala	Lys				
305					310					315					320				
Glu	Glu	Asp	Asp	Tyr	Asp	Val	Met	Gln	Asp	Pro	Glu	Phe	Leu	Gln	Ser				
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Val	Leu	Glu	Asn	Leu	Pro	Gly	Val	Asp	Pro	Asn	Asn	Glu	Ala	Ile	Arg				
			340					345					350						
Asn	Ala	Met	Gly	Ser	Leu	Pro	Pro	Arg	Pro	Pro	Arg	Thr	Ala	Arg	Arg				
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 <213> Homo sapiens

 <220>
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 <222> (63)..(1208)

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Met Val Leu Glu Ser Thr Met Val Cys Val Asp Asn Ser Glu Tyr
1 5 10 15

atg cgg aat gga gac ttc tta ccc acc agg ctg cag gcc cag cag gat 155
Met Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp
20 25 30

gct gtc aac ata gtt tgt cat tca aag acc cgc agc aac cct gag aac 203
Ala Val Asn Ile Val Cys His Ser Lys Thr Arg Ser Asn Pro Glu Asn
35 40 45

aac gtg ggc ctt atc aca ctg gct aat gac tgt gaa gtg ctg acc aca 251
Asn Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr
50 55 60

ctc acc cca gac act ggc cgt atc ctg tcc aag cta cat act gtc caa 299
Leu Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln
65 70 75

ccc aag ggc aag atc acc ttc tgc acg ggc atc cgc gtg gcc cat ctg 347
Pro Lys Gly Lys Ile Thr Phe Cys Thr Gly Ile Arg Val Ala His Leu
80 85 90 95

gct ctg aag cac cga caa ggc aag aat cac aag atg cgc atc att gcc 395
Ala Leu Lys His Arg Gln Gly Lys Asn His Lys Met Arg Ile Ile Ala
100 105 110

ttt gtg gga agc cca gtg gag gac aat gag aag gat ctg gtg aaa ctg 443
Phe Val Gly Ser Pro Val Glu Asp Asn Glu Lys Asp Leu Val Lys Leu
115 120 125

gct aaa cgc ctc aag aag gag aaa gta aat gtt gac att atc aat ttt 491
Ala Lys Arg Leu Lys Lys Glu Lys Val Asn Val Asp Ile Ile Asn Phe
130 135 140

ggg gaa gag gag gtg aac aca gaa aag ctg aca gcc ttt gta aac acg 539
Gly Glu Glu Glu Val Asn Thr Glu Lys Leu Thr Ala Phe Val Asn Thr
145 150 155

ttg aat ggc aaa gat gga acc ggt tct cat ctg gtg aca gtg cct cct 587
Leu Asn Gly Lys Asp Gly Thr Gly Ser His Leu Val Thr Val Pro Pro
160 165 170 175

ggg ccc agt ttg gct gat gct ctc atc agt tct ccg att ttg gct ggt 635
Gly Pro Ser Leu Ala Asp Ala Leu Ile Ser Ser Pro Ile Leu Ala Gly
180 185 190

gaa ggt ggt gcc atg ctg ggt ctt ggt gcc agt gac ttt gaa ttt gga 683
Glu Gly Gly Ala Met Leu Gly Leu Gly Ala Ser Asp Phe Glu Phe Gly
195 200 205

gta gat ccc agt gct gat cct gag ctg gcc ttg gcc ctt cgt gta tct 731
Val Asp Pro Ser Ala Asp Pro Glu Leu Ala Leu Ala Leu Arg Val Ser

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Met Glu Glu Gln Arg His Ala Gly Gly Gly Ala Arg Arg Ala Ala Arg			
225	230	235	
gct tct gct gct gag gcc ggg att gct acg act ggg act gaa gac tca			827
Ala Ser Ala Ala Glu Ala Gly Ile Ala Thr Thr Gly Thr Glu Asp Ser			
240	245	250	255
gac gat gcc ctg ctg aag atg acc atc agc cag caa gag ttt ggc cgc			875
Asp Asp Ala Leu Leu Lys Met Thr Ile Ser Gln Gln Glu Phe Gly Arg			
260	265	270	
act ggg ctt cct gac cta agc agt agt act gag gaa gag gag att gct			923
Thr Gly Leu Pro Asp Leu Ser Ser Ser Thr Glu Glu Glu Glu Ile Ala			
275	280	285	
tat gcc atg cag atg tcc ctg cag gga gca gag ttt ggc cag gcg gaa			971
Tyr Ala Met Gln Met Ser Leu Gln Gly Ala Glu Phe Gly Gln Ala Glu			
290	295	300	
tca gca gac att gat gcc agc tca gct atg gac aca tct gag cca gcc			1019
Ser Ala Asp Ile Asp Ala Ser Ser Ala Met Asp Thr Ser Glu Pro Ala			
305	310	315	
aag gag gag gat gat tac gac gtg atg cag gac ccc gag ttc ctt cag			1067
Lys Glu Glu Asp Asp Tyr Asp Val Met Gln Asp Pro Glu Phe Leu Gln			
320	325	330	335
agt gtc cta gag aac ctc cca ggt gtg gat ccc aac aat gaa gcc att			1115
Ser Val Leu Glu Asn Leu Pro Gly Val Asp Pro Asn Asn Glu Ala Ile			
340	345	350	
cga aat gct atg ggc tcc ctg cct ccc agg cca cca agg acg gca aga			1163
Arg Asn Ala Met Gly Ser Leu Pro Pro Arg Pro Pro Arg Thr Ala Arg			
355	360	365	
agg aca aga agg agg aag aca aga agt gag act gga ggg aaa ggg			1208
Arg Thr Arg Arg Arg Lys Thr Arg Ser Glu Thr Gly Gly Lys Gly			
370	375	380	
tagctgagtc tgcttagggg actgggaagc acggaatata gggttagatg tggttatctg			1268
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<211> 46

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
amino acid sequence

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<222> (1)..(35)
<223> This region may or may not be present

<220>
<221> MOD_RES
<222> (38)
<223> His, Arg or Lys

<220>
<221> MOD_RES
<222> (39)
<223> Ser or Leu

<220>
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<223> Thr or Ala

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<223> This region may or may not be present

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Val Asn Ile Val Cys Xaa Xaa Lys Xaa Arg Ser Asn Pro Glu
35 40 45

<210> 4
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<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
amino acid sequence

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<223> This region may or may not be present

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<223> Thr or Ala

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<222> (43)..(51)

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Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp Ala
20 25 30

Val Asn Ile Val Cys Xaa Xaa Lys Xaa Arg Ser Asn Pro Glu Asn Asn
35 40 45

Val Gly Leu
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<211> 80

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
amino acid sequence

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<221> MOD_RES

<222> (1)..(35)

<223> This region may or may not be present

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<221> MOD_RES

<222> (38)

<223> His, Arg or Lys

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<222> (39)

<223> Ser or Leu

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<223> Thr or Ala

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<223> This region may or may not be present

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Arg	Asn	Gly	Asp	Phe	Leu	Pro	Thr	Arg	Leu	Gln	Ala	Gln	Gln	Asp	Ala
			20					25					30		

Val	Asn	Ile	Val	Cys	Xaa	Xaa	Lys	Xaa	Arg	Ser	Asn	Pro	Glu	Asn	Asn
		35					40					45			

Val	Gly	Leu	Ile	Thr	Leu	Ala	Asn	Asp	Cys	Glu	Val	Leu	Thr	Thr	Leu
	50					55						60			

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<212> PRT

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amino acid sequence

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<223> This region may or may not be present

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<223> His, Arg or Lys

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<223> Thr or Ala

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<223> This region may or may not be present

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Arg	Asn	Gly	Asp	Phe	Leu	Pro	Thr	Arg	Leu	Gln	Ala	Gln	Gln	Asp	Ala			
			20					25					30					
Val	Asn	Ile	Val	Cys	Xaa	Xaa	Lys	Xaa	Arg	Ser	Asn	Pro	Glu	Asn	Asn			
			35				40					45						
Val	Gly	Leu	Ile	Thr	Leu	Ala	Asn	Asp	Cys	Glu	Val	Leu	Thr	Thr	Leu			
		50				55					60							
Thr	Pro	Asp	Thr	Gly	Arg	Ile	Leu	Ser	Lys	Leu	His	Thr	Val	Gln	Pro			
	65				70					75					80			
Lys	Gly	Lys	Ile	Thr	Phe	Cys	Thr	Gly	Ile	Arg	Val	Ala	His	Leu	Ala			
				85					90					95				
Leu	Lys	His	Arg	Gln	Gly	Lys	Asn	His	Lys	Met	Arg	Ile	Ile	Ala	Phe			
			100					105					110					
Val	Gly	Ser	Pro	Val	Glu	Asp	Asn	Glu	Lys	Asp	Leu	Val	Lys	Leu	Ala			
		115					120					125						
Lys	Arg	Leu	Lys	Lys	Glu	Lys	Val	Asn	Val	Asp	Ile	Ile	Asn	Phe	Gly			
	130					135					140							
Glu	Glu	Glu	Val	Asn	Thr	Glu	Lys	Leu	Thr	Ala	Phe	Val	Asn	Thr	Leu			
	145				150				155						160			
Asn	Gly	Lys																